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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: markspencer

Timestamp: [year=2010; month=3; day=16; hr=7; min=57; sec=39; ms=774;]

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Reviewer Comments:

1.

W402 Undefined organism found in <213> in SEQ ID (1)
E311 Invalid field content in <220> in SEQ ID (1)
E257 Invalid sequence data feature in <221> in SEQ ID (1)
W401 Unrecognized range formatin <222> in SEQID (1)
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W401 Unrecognized range formatin <222> in SEQID (19)
W402 Undefined organism found in <213> in SEQ ID (20) This
error has occured more than 20 times, will not be displayed
E311 Invalid field content in <220> in SEQ ID (20) This error
has occured more than 20 times, will not be displayed
E257 Invalid sequence data feature in <221> in SEQ ID (20)
This error has occured more than 20 times, will not be displayed
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error has occured more than 20 times, will not be displayed

<210> 1
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<212> DNA
<213> ORGANISM: ARTIFICIAL SEQUENCE
<220> FEATURE
<221> NAME/KEY: Modified-base
<222> LOCATION: (1), (2), (3), (13), (14), (15)
<223> OTHER INFORMATION: beta-D-amino-LNA Monomer
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For SEQ ID # 1 through 30, please remove all subject line headers from
the entire sequence listing. Example: "<213> ORGANISM: ARTIFICIAL
SEQUENCE" should be "<213> ARTIFICIAL SEQUENCE". Please remove subject
line headers "FEATURE", "NAME/KEY:", "LOCATION:", and "OTHER
INFORMATION:" from numeric identifiers <220>, <221>, <222>, and <223>
respectively. Please make all necessary changes.

For SEQ ID # 1 through 30, when using "Artificial sequence", for numeric
identifier <213>, a mandatory feature is required to explain the source
of the genetic material. The feature consists of numeric identifier
<220>, which remains blank and numeric identifier <223>, which states
the source of the genetic material. To explain the source, if the
sequence is put together from several organisms, please list those
organisms. If the sequence is made in the laboratory, please indicate
that the sequence is synthesized. Please make all necessary changes.

Application No: 10535472 Version No: 1.0

Input Set:

Output Set:

Started: 2010-03-03 18:40:07.002
Finished: 2010-03-03 18:40:29.095
Elapsed: 0 hr(s) 0 min(s) 22 sec(s) 93 ms
Total Warnings: 60
Total Errors: 60
No. of SeqIDs Defined: 30
Actual SeqID Count: 30

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E 257	Invalid sequence data feature in <221> in SEQ ID (1)
W 401	Unrecognized range formatin <222> in SEQID (1)
W 402	Undefined organism found in <213> in SEQ ID (2)
E 311	Invalid field content in <220> in SEQ ID (2)
E 257	Invalid sequence data feature in <221> in SEQ ID (2)
W 401	Unrecognized range formatin <222> in SEQID (2)
W 402	Undefined organism found in <213> in SEQ ID (3)
E 311	Invalid field content in <220> in SEQ ID (3)
E 257	Invalid sequence data feature in <221> in SEQ ID (3)
W 401	Unrecognized range formatin <222> in SEQID (3)
W 402	Undefined organism found in <213> in SEQ ID (4)
E 311	Invalid field content in <220> in SEQ ID (4)
E 257	Invalid sequence data feature in <221> in SEQ ID (4)
W 401	Unrecognized range formatin <222> in SEQID (4)
W 402	Undefined organism found in <213> in SEQ ID (5)
E 311	Invalid field content in <220> in SEQ ID (5)
E 257	Invalid sequence data feature in <221> in SEQ ID (5)
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Input Set:

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Finished: 2010-03-03 18:40:29.095
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E 311	Invalid field content in <220> in SEQ ID (6)
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W 402	Undefined organism found in <213> in SEQ ID (7)
E 311	Invalid field content in <220> in SEQ ID (7)
E 257	Invalid sequence data feature in <221> in SEQ ID (7)
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W 401	Unrecognized range formatin <222> in SEQID (8)
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W 402	Undefined organism found in <213> in SEQ ID (10)
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E 257	Invalid sequence data feature in <221> in SEQ ID (10)
W 401	Unrecognized range formatin <222> in SEQID (10)
W 402	Undefined organism found in <213> in SEQ ID (11)
E 311	Invalid field content in <220> in SEQ ID (11)

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W 401	Unrecognized range formatin <222> in SEQID (13)
W 402	Undefined organism found in <213> in SEQ ID (14)
E 311	Invalid field content in <220> in SEQ ID (14)
E 257	Invalid sequence data feature in <221> in SEQ ID (14)
W 401	Unrecognized range formatin <222> in SEQID (14)
W 402	Undefined organism found in <213> in SEQ ID (15)
E 311	Invalid field content in <220> in SEQ ID (15)
E 257	Invalid sequence data feature in <221> in SEQ ID (15)
W 401	Unrecognized range formatin <222> in SEQID (15)
W 402	Undefined organism found in <213> in SEQ ID (16)
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Input Set:

Output Set:

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Total Errors: 60
No. of SeqIDs Defined: 30
Actual SeqID Count: 30

Error code	Error Description
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E 311	Invalid field content in <220> in SEQ ID (17)
E 257	Invalid sequence data feature in <221> in SEQ ID (17)
W 401	Unrecognized range formatin <222> in SEQID (17)
W 402	Undefined organism found in <213> in SEQ ID (18)
E 311	Invalid field content in <220> in SEQ ID (18)
E 257	Invalid sequence data feature in <221> in SEQ ID (18)
W 401	Unrecognized range formatin <222> in SEQID (18)
W 402	Undefined organism found in <213> in SEQ ID (19)
E 311	Invalid field content in <220> in SEQ ID (19)
E 257	Invalid sequence data feature in <221> in SEQ ID (19)
W 401	Unrecognized range formatin <222> in SEQID (19)
W 402	Undefined organism found in <213> in SEQ ID (20) This error has occured more than 20 times, will not be displayed
E 311	Invalid field content in <220> in SEQ ID (20) This error has occured more than 20 times, will not be displayed
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W 401	Unrecognized range formatin <222> in SEQID (20) This error has occured more than 20 times, will not be displayed

SEQUENCE LISTING

<110> Christenson, Signe M.
Mikkelsen, Nikolaj D.
Frieden, Miriam
Hansen, Henrik F.
Koch, Troels
Pedersen, Daniel S.
Rosenbohm, Christoph
Thrue, Charlotte A.
Westergaard, Majken

<120> AMINO-LNA, THIO-LNA and ALPHA-L-OXY-LNA

<130> 22460-0003US1

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<141> 2010-03-03

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<151> 2003-11-18

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<222> LOCATION: (1), (2), (3), (13), (14), (15)
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